

## SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.  
 Hannah, L. Curtis  
 Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose  
 Pyrophosphorylase

<130> UF.371XC1

<140> 10/569,000

<141> 2006-10-10

<150> PCT/US2004/026965

<151> 2004-08-18

<150> 60/496,188

<151> 2003-08-18

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<170> PatentIn version 3.2

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Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala	Ala
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Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala					
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Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile					
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg					
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          20          25          30

Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
          35          40          45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
          50          55          60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65          70          75          80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
          85          90          95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
          100          105          110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu

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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn 145 150 155 160		
Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp 165 170 175		
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr 180 185 190		
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu 195 200 205		
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro 210 215 220		
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly 225 230 235 240		
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly 245 250 255		
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln 260 265 270		
Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr 275 280 285		
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu 290 295 300		
Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr 305 310 315 320		
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile 325 330 335		
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp 340 345 350		
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys 355 360 365		
Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala 370 375 380		
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu 385 390 395 400		
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile 405 410 415		
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg		

420                      425                      430  
 Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala  
           435                      440                      445  
 Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val  
           450                      455                      460  
 Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile  
 465                      470                      475

<210> 9  
 <211> 1428  
 <212> DNA  
 <213> zea mays

<400> 9  
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 cagccaattc caaagcgtga caaagccgct gcaaagtatt caagarcatt yctcaatcct 120  
 caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac 180  
 cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt 240  
 gatattcctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa 300  
 tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg 360  
 tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac 420  
 tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat 480  
 gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc 540  
 attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag 600  
 aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aaggaggat cattgagttt 660  
 gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc 720  
 cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc 780  
 agcaaagatg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga 840  
 agtgagggtta ttccaggtgc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat 900  
 ggttactggg aagatatcgg taccattgag gcattttata atgcaaactt gggaataacc 960  
 aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct 1020  
 cgacacctgc caccttcaaa ggttottgat gctgatgtga cagacagtgt tattgggtgaa 1080  
 ggatgtgtta ttaaaaaactg caagataaac cattctgtag ttggactccg atcttgcata 1140  
 tctgaagggtg ctatcataga ggacagttta ctaatgggtg cggactacta tgagacagaa 1200

gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca 1260  
 tgcatacagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc 1320  
 aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaagggtgga 1380  
 attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata 1428

<210> 10  
 <211> 476  
 <212> PRT  
 <213> zea mays

<400> 10

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala  
 1 5 10 15  
 Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn  
 20 25 30  
 Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly  
 35 40 45  
 Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys  
 50 55 60  
 Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile  
 65 70 75 80  
 Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr  
 85 90 95  
 Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg  
 100 105 110  
 Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu  
 115 120 125  
 Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly  
 130 135 140  
 Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn  
 145 150 155 160  
 Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp  
 165 170 175  
 Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr  
 180 185 190  
 Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu  
 195 200 205  
 Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro

210					215					220					
Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly
225					230					235					240
Leu	Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met	Gly
				245					250					255	
Ile	Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln
			260					265					270		
Phe	Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr
		275					280					285			
Ser	Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu
	290					295					300				
Asp	Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr
305						310					315				320
Lys	Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile
				325					330					335	
Tyr	Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp
			340						345				350		
Val	Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys
		355					360					365			
Ile	Asn	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly	Ala
	370					375					380				
Ile	Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu
385						390					395				400
Ala	Asp	Lys	Lys	Leu	Leu	Ala	Glu	Lys	Gly	Gly	Ile	Pro	Ile	Gly	Ile
				405					410					415	
Gly	Lys	Asn	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala	Arg
				420				425					430		
Ile	Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala
	435						440					445			
Ala	Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val
	450					455					460				
Ile	Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile				
465						470					475				

<210> 11  
 <211> 1582  
 <212> DNA  
 <213> Zea mays

<220>

<221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1578)  
 <223> k = g or t.

<400> 11  
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
           Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
           1                  5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
           35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
           50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
           65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
   80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
   95                  100                  105                  110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
           115                  120                  125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
           130                  135                  140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150						155				
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
175					180					185					190		
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195					200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240					245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
255					260					265					270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275					280					285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305					310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	cat	agt	1011	
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser		
	320					325						330					
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
335					340					345					350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355				360						365			
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155	
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys		



370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg			1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca			1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala			
495	500	505	510
acc atc aac gat ggg tct gtc ata tagatcggct gcgktktgcg			1582
Thr Ile Asn Asp Gly Ser Val Ile			
515			

<210> 12  
 <211> 518  
 <212> PRT  
 <213> Zea mays

<400> 12

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile			
1	5	10	15
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile			
20	25	30	
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly			
35	40	45	
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro			
50	55	60	

Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270	
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	275	280	285	
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	290	295	300	
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp	305	310	315	320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln	325	330	335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser	340	345	350	
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp	355	360	365	

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser  
 485 490 495  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 500 505 510  
 Asn Asp Gly Ser Val Ile  
 515

<210> 13  
 <211> 1582  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1578)

&lt;223&gt; k = g or t.

&lt;400&gt; 13

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
           1                          5                          10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                          20                          25                          30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                           35                          40                          45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                           50                          55                          60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                           65                          70                          75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
   80                          85                          90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
   95                          100                          105                          110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
                           115                          120                          125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
                           130                          135                          140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
                           145                          150                          155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
   160                          165                          170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
   175                          180                          185                          190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220			675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235			723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250			771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270			819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285			867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300			915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315			963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320 325 330			1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350			1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365			1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380			1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395			1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410			1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430			1299

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445  
  
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460  
  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475  
  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490  
  
 tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539  
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala  
 495 500 505 510  
  
 acc atc aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1582  
 Thr Ile Asn Asp Gly Ser Val Ile  
 515

<210> 14

<211> 518

<212> PRT

<213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15  
  
 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30  
  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
           435                                  440                                  445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
           450                                  455                                  460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
           465                                  470                                  475                                  480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser  
                                   485                                  490                                  495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
                                   500                                  505                                  510

Asn Asp Gly Ser Val Ile  
                                   515

<210> 15

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be  
           heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 15

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
           Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
                   1                                  5                                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
           Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu



15	20	25	30	
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt				147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	35	40	45	
ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct				195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat				243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga				291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	80	85	90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct				339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc				387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act				435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac				483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa				531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt				579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att				627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	250	

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 16  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 16

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

195	200	205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln		
210	215	220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val		
225	230	235 240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr		
	245	250 255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
	260	265 270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
	275	280 285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
	290	295 300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315 320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln		
	325	330 335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
	340	345 350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
	355	360 365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
	370	375 380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
	405	410 415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
	420	425 430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435	440 445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450	455 460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
	485	490 495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		

500

505

510

Gly Ser Val Ile  
515

&lt;210&gt; 17

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be  
heat stable

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (267)

&lt;223&gt; k = g or t; amino acid 86 = Ala.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (540)

&lt;223&gt; n = a or g or c or t/u, unknown, or other.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1008)

&lt;223&gt; y = c or t.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1368)

&lt;223&gt; r = a or g; amino acid 453 = Pro.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1572)

&lt;223&gt; k = g or t.

&lt;400&gt; 17

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat			243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr			
65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga			291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly			
80	85	90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct			339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro			
95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc			387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act			435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac			483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160	165	170	
gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510	1539

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 Asn Asp Gly Ser Val Ile  
 515

1576

<210> 18  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 18

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr



	245		250		255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn					
	260		265		270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala					
	275		280		285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys					
	290		295		300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp					
	305		310		315
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln					
	325		330		335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser					
	340		345		350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp					
	355		360		365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro					
	370		375		380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp					
	385		390		395
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val					
	405		410		415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met					
	420		425		430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu					
	435		440		445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn					
	450		455		460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr					
	465		470		475
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr					
	485		490		495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp					
	500		505		510
Gly Ser Val Ile					
	515				

&lt;210&gt; 19

&lt;211&gt; 1576

&lt;212&gt; DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1209)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1371)

<223> h = a or c or t/u.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 19

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5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga			291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly			
80	85	90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct			339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro			
95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc			387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
	115	120	125
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act			435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
	130	135	140
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac			483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
	145	150	155
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
	160	165	170
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
	175	180	185
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
	195	200	205
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
	210	215	220
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
	225	230	235
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
	240	245	250
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
	255	260	265
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
	290	295	300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	
495 500 505 510	
aac gat ggg tct gtc ata tagatcggt gcgktgtcg	1576
Asn Asp Gly Ser Val Ile	
515	

<210> 20  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 20

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
      50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
      65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
      85              90              95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
      100             105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
      115             120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
      130             135             140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
      145             150             155             160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
      165             170             175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
      180             185             190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
      195             200             205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
      210             215             220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
      225             230             235             240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
      245             250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn

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260	265	270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
275	280	285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln		
325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
340	345	350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His		
385	390	395
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
405	410	415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
420	425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
435	440	445
Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
450	455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
485	490	495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
500	505	510
Gly Ser Val Ile		
515		

<210> 21  
 <211> 1576  
 <212> DNA  
 <213> Zea mays

<220>

<221> CDS  
 <222> (10)..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (321)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

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                   1                  5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                   35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                   50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                   65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
                   80                  85                  90

tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro

95	100	105	110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc				387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe				
	115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act				435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr				
	130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac				483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn				
	145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa				531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu				
	160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt				579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe				
	175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att				627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile				
	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu				
	210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala				
	225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp				
	240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat				819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp				
	255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat				867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp				
	275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc				915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe				
	290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta				963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu				
	305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt				1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser				
	320	325	330	



gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059  
 Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile  
 335 340 345 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107  
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys  
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile  
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

&lt;210&gt; 22

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 22

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15  
 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
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 Gly Ser Val Ile  
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<210> 23

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

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<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

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<222> (1389)

<223> h = a or c or t/u.

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10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac			483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
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gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
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Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
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cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
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His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305	310	315	
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His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
355	360	365	

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Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtgcg 1576
Asn Asp Gly Ser Val Ile
515

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
          35           40           45

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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
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 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
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 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
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 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
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 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
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 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
                                   405                                  410                                  415  
  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
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 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
           435                                  440                                  445  
  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn  
           450                                  455                                  460  
  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465                                  470                                  475                                  480  
  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
                                   485                                  490                                  495  
  
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 Gly Ser Val Ile  
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<213> Zea mays

<220>

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<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

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<222> (657)

<223> n = a or g or c or t/u, unknown, or other.

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<221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
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 <223> r = a or g; amino acid 453 = Pro.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                           35                          40                          45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                           50                          55                          60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                           65                          70                          75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
           80                          85                          90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
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aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
                           130                          135                          140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
                           145                          150                          155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160	165	170	
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Glu Pro Ala Gly Trp Phe	Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe		
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
	195	200	205
gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu			
	210	215	220
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
	225	230	235
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
	240	245	250
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
	255	260	265
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
	290	295	300
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
	305	310	315
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
	320	325	330
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
	335	340	345
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
	355	360	365
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			
	370	375	380
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
	385	390	395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
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 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
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 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
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ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
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 450 455 460

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 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

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 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

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 Asn Asp Gly Ser Val Ile  
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln

85																90																95																																															
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly																																																																
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Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser																																																																
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Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu																																																																
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Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala																																																																
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Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro																																																																
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Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp																																																																
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Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile																																																																
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Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val																																																																
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Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr																																																																
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Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn																																																																
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Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala																																																																
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Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys																																																																
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Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln																																																																
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Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser																																																																
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Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp																																																																
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Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro																																																																
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Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp																																																																

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385              390              395              400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
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Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
              420              425              430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
              435              440              445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
              450              455              460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465              470              475              480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
              485              490              495
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<210> 27

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<212> DNA

<213> Zea mays

<220>

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<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

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<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

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<223> y = c or t.

<220>

<221> variation

<222> (1287)

<223> y = c or t.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1368)

&lt;223&gt; r = a or g; amino acid 453 = Pro.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1572)

&lt;223&gt; k = g or t.

&lt;400&gt; 27

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145

150

155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531

Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160

165

170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251

Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410  
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val  
 415 420 425 430  
 atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu  
 435 440 445  
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490  
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510  
 aac gat ggg tct gtc ata tagatcggct gcgktgtgct 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 28  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 28

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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 20 25 30  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95



Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
                     405                    410                    415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met  
                     420                    425                    430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
                     435                    440                    445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
                     450                    455                    460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
                     465                    470                    475                    480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
                     485                    490                    495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
                     500                    505                    510  
 Gly Ser Val Ile  
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<210> 29  
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 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form, modified to be  
         heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
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 <222> (981)  
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<220>  
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 <222> (1008)  
 <223> y = c or t.

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 <222> (1086)  
 <223> n = a or g or c or t/u, unknown, or other.

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<221> variation  
 <222> (1197)  
 <223> n = a or g or c or t/u, unknown, or other.

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 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
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 <222> (1572)  
 <223> k = g or t.

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 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
           Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
           1                          5                          10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                          20                          25                          30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                           35                          40                          45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                           50                          55                          60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                           65                          70                          75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
           80                          85                          90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
   95                          100                          105                          110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
                           115                          120                          125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
                           130                          135                          140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
                           145                          150                          155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160	165	170	
gag cca gct gga tgg ttc	cag ggt aca gca gac	tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe	Gln Gly Thr Ala Asp	Ser Ile Arg Lys Phe	
175	180	185 190	
atc tgg gta ctc gag gat	tat tac agt cac aaa	tcc att gac aac att	627
Ile Trp Val Leu Glu Asp	Tyr Tyr Ser His Lys	Ser Ile Asp Asn Ile	
195	200	205	
gta atc ttg agt ggc gat	cag ctt tat cgg atg	aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp	Gln Leu Tyr Arg Met	Asn Tyr Met Glu Leu	
210	215	220	
gtg cag aaa cat gtc gag	gac gat gct gat atc	act ata tca tgt gct	723
Val Gln Lys His Val Glu	Asp Asp Ala Asp Ile	Thr Ile Ser Cys Ala	
225	230	235	
cct gtt gat gag agc cga	gct tct aaa aat ggg	cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg	Ala Ser Lys Asn Gly	Leu Val Lys Ile Asp	
240	245	250	
cat act gga cgt gta ctt	caa ttc ttt gaa aaa	cca aag ggt gct gat	819
His Thr Gly Arg Val Leu	Gln Phe Phe Glu Lys	Pro Lys Gly Ala Asp	
255	260	265 270	
ttg aat tct atg aga gtt	gag acc aac ttc ctg	agc tat gct ata gat	867
Leu Asn Ser Met Arg Val	Glu Thr Asn Phe Leu	Ser Tyr Ala Ile Asp	
275	280	285	
gat gca cag aaa tat cca	tac ctt gca tca atg	ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro	Tyr Leu Ala Ser Met	Gly Ile Tyr Val Phe	
290	295	300	
aag aaa gat gca ctt tta	gac ctt ctc aag tca	aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu	Asp Leu Leu Lys Ser	Lys Tyr Thr Gln Leu	
305	310	315	
cat gac ttt gga tct aar	atc ctc cca aga gct	gta cta gat cay agt	1011
His Asp Phe Gly Ser Lys	Ile Leu Pro Arg Ala	Val Leu Asp His Ser	
320	325	330	
gtg cag gca tgc att ttt	acg ggc tat tgg gag	gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe	Thr Gly Tyr Trp Glu	Asp Val Gly Thr Ile	
335	340	345 350	
aaa tca ttc ttt gat gca	aac ttg gtn ctc act	gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala	Asn Leu Val Leu Thr	Glu Gln Pro Ser Lys	
355	360	365	
ttt gat ttt tac gat cca	aaa aca cct ttc ttc	act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro	Lys Thr Pro Phe Phe	Thr Ala Pro Arg Cys	
370	375	380	
ttg cct ccg acg caa ttg	gac aag tgc aag atg	aaa tat gtn ttt atc	1203
Leu Pro Pro Thr Gln Leu	Asp Lys Cys Lys Met	Lys Tyr Val Phe Ile	
385	390	395	

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 30  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 30

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln

85				90				95							
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100												110
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
			115				120								125
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
			130				135								140
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
															160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
															175
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180												190
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
			195												205
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
			210												220
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
															240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
															255
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260												270
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
			275												285
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
			290												300
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
															320
Phe	Gly	Ser	Lys	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
															335
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
			340												350
Phe	Phe	Asp	Ala	Asn	Leu	Val	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
			355												365
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro
			370												380
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Val	Phe	Ile	Ser	Asp

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385          390          395          400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
      405          410          415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
      420          425          430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435          440          445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
      450          455          460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465          470          475          480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
      485          490          495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
      500          505          510
Gly Ser Val Ile
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<210> 31
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<212> DNA
<213> Zea mays

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<220>
<221> CDS
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<223> Shrunk-2 gene revertant form, modified to be
      heat stable

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<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

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```

<220>
<221> variation
<222> (1008)
<223> y = c or t.

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<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

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<220>
<221> variation
<222> (1572)
<223> k = g or t.

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&lt;400&gt; 31

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          1              5              10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20              25              30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35              40              45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50              55              60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65              70              75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80              85              90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95              100              105              110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115              120              125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130              135              140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
          145              150              155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
          160              165              170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
          175              180              185              190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
          195              200              205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
          210              215              220

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gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tty agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
                   450                  455                  460  
  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
                   465                  470                  475  
  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
                   480                  485                  490  
  
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
                   495                  500                  505                  510  
  
 aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1576  
 Asn Asp Gly Ser Val Ile  
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<210> 32  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 32

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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                   20                  25                  30  
  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
                   35                  40                  45  
  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
                   50                  55                  60  
  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
                   65                  70                  75                  80  
  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
                   85                  90                  95  
  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
                   100                  105                  110  
  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
                   115                  120                  125  
  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
                   130                  135                  140  
  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
                   145                  150                  155                  160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495  
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 500 505 510  
 Gly Ser Val Ile  
 515

<210> 33  
 <211> 1576  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
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 <222> (1572)  
 <223> k = g or t.

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 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65 70 75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	
80 85 90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915

Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
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Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	
495 500 505 510	
aac gat ggg tct gtc ata tagatcggct gcgktg	1576
Asn Asp Gly Ser Val Ile	

515

&lt;210&gt; 34

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 34

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          20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
          35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
  50              55              60

Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
  65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Gly  Thr  Gly  Ser  Gln
          85              90              95

Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100             105             110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115             120             125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
          130             135             140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Gly  Ile  Asn  Phe  Ala
          145             150             155             160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
          165             170             175

Ala  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180             185             190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
          195             200             205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210             215             220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
          225             230             235             240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245             250             255

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Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
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<210> 35  
 <211> 1576  
 <212> DNA  
 <213> Zea mays



<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunk-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (540)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
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 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
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 <223> k = g or t.

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                   1                  5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                   35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                   50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                   65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
                   80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
ggt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011

His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser  
 320 325 330  
 gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059  
 Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile  
 335 340 345 350  
 aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107  
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys  
 355 360 365  
 ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380  
 ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile  
 385 390 395  
 tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410  
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430  
 atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445  
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490  
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510  
 aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 36  
 <211> 516  
 <212> PRT  
 <213> Zea mays

&lt;400&gt; 36

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
      20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
      85              90              95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
      100              105              110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
      115              120              125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
      130              135              140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
      145              150              155              160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
      165              170              175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
      180              185              190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
      195              200              205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
      210              215              220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
      225              230              235              240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
      245              250              255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
      260              265              270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
      275              280              285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys

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290	295	300
Asp Ala Leu Leu Asp	Leu Leu Lys Ser Lys	Tyr Thr Gln Leu His Asp
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Phe Gly Ser Glu Ile	Leu Pro Arg Ala Val	Leu Asp Tyr Ser Val Gln
	325	330 335
Ala Cys Ile Phe Thr	Gly Tyr Trp Glu Asp	Val Gly Thr Ile Lys Ser
	340	345 350
Phe Phe Asp Ala Asn	Leu Ala Leu Thr	Glu Gln Pro Ser Lys Phe Asp
	355	360 365
Phe Tyr Asp Pro Lys	Thr Pro Phe Phe Thr	Ala Pro Arg Cys Leu Pro
	370	375 380
Pro Thr Gln Leu Asp	Lys Cys Lys Met Lys	Tyr Ala Phe Ile Ser Asp
	385	390 395 400
Gly Cys Leu Leu Arg	Glu Cys Asn Ile Glu	His Ser Val Ile Gly Val
	405	410 415
Cys Ser Arg Val Ser	Ser Gly Cys Glu Leu	Lys Asp Ser Val Met Met
	420	425 430
Gly Ala Asp Ile Tyr	Glu Thr Glu Glu Ala	Ser Lys Leu Leu Leu
	435	440 445
Ala Gly Lys Val Pro	Val Gly Ile Gly Arg	Asn Thr Lys Ile Arg Asn
	450	455 460
Cys Ile Ile Asp Met	Asn Ala Arg Ile Gly	Lys Asn Val Val Ile Thr
	465	470 475 480
Asn Ser Lys Gly Ile	Gln Glu Ala Asp His	Pro Glu Glu Gly Tyr Tyr
	485	490 495
Ile Arg Ser Gly Ile	Val Val Ile Leu Lys	Asn Ala Thr Ile Asn Asp
	500	505 510
Gly Ser Val Ile		
	515	

&lt;210&gt; 37

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
heat stable

&lt;220&gt;

<221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1197)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

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                   1                  5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                   35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                   50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                   65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
                   80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
                   95                  100                  105                  110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
                   115                  120                  125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107

Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys  
 355 360 365  
 ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380  
 ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile  
 385 390 395  
 tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410  
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430  
 atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445  
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490  
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510  
 aac gat ggg tct gtc ata tagatcggct gcgktktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 38  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 38

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15  
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 20 25 30



Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
                   35                                  40                                  45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
                   50                                  55                                  60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
                   65                                  70                                  75                                  80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
                                   85                                  90                                  95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
                                   100                                  105                                  110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
                   115                                  120                                  125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
                   130                                  135                                  140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
                   145                                  150                                  155                                  160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
                                   165                                  170                                  175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
                                   180                                  185                                  190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
                   195                                  200                                  205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
                   210                                  215                                  220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
                   225                                  230                                  235                                  240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
                                   245                                  250                                  255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
                                   260                                  265                                  270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
                   275                                  280                                  285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
                   290                                  295                                  300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
                   305                                  310                                  315                                  320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
                                   325                                  330                                  335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
                   340                  345                  350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
                   355                  360                  365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
                   370                  375                  380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp  
                   385                  390                  395                  400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
                   405                  410                  415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
                   420                  425                  430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
                   435                  440                  445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
                   450                  455                  460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
                   465                  470                  475                  480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
                   485                  490                  495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
                   500                  505                  510

Gly Ser Val Ile  
                   515

<210> 39

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be  
           heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1197)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

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                   1                  5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
   15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
                   35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
                   50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
                   65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
                   80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
                   95                  100                  105                  110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
                   115                  120                  125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
                   130                  135                  140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile  
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

&lt;210&gt; 40

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 40

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

50					55					60					
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
65					70					75					80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
				85					90					95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
		115					120					125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
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Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
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Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
				165					170					175	
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225					230					235					240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
			275				280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290					295					300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310					315					320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
				325					330					335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
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Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp

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<210> 41
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
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<223> y = c or t.

<220>

<221> variation

<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145

150

155



ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
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Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
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Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	

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 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile  
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

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 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

&lt;210&gt; 42

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 42

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

65		70		75		80
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln						
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Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly						
	100			105		110
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser						
	115			120		125
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu						
	130			135		140
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala						
	145			150		155
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro						
	165			170		175
Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp						
	180			185		190
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile						
	195			200		205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln						
	210			215		220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val						
	225			230		235
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr						
	245			250		255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn						
	260			265		270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala						
	275			280		285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys						
	290			295		300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp						
	305			310		315
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln						
	325			330		335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser						
	340			345		350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp						
	355			360		365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro						

370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp		
385	390	395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
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Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
	420	425 430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435	440 445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450	455 460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
	485	490 495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
	500	505 510
Gly Ser Val Ile		
	515	